

# WEST Search History

DATE: Tuesday, January 07, 2003

## Set Name Query

side by side

## Hit Count Set Name

result set

*DB=USPT,PGPB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=OR*

L8	L7 and (@PD<19961028 or @RLAD<19961028)	10	L8
L7	(2D7 or PA14) and (chemokine or HIV)	105	L7
L6	(HDG NR10 or 88-C) and chemokine	20	L6
L5	L4 and (@PD<19961028 or @RLAD<19961028)	40	L5
L4	L3 and antibody	455	L4
L3	L2 and chemokine	588	L3
L2	(CCR5 or CC-CkR5 or CCCKR5 or CKR5 or ChemR13 or CMKBR5 or CCR-5)	706	L2

*DB=USPT; THES=ASSIGNEE; PLUR=YES; OP=OR*

L1	5939320.pn. or 5994515.pn. or 6025154.pn.	3	L1
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END OF SEARCH HISTORY



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## SEARCH GeneCards


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### RESULT:

5 GeneCards match **your precise query** for "CCR5";

Each is represented by a minicard.

Click "Display" on the left to get the full GeneCard.

**Display**  
the complete  
GeneCard  
for this  
gene  
(CCR5)

**More like this**

**Gene:** CCR5 = chemokine (C-C motif) receptor 5 [Locus: 3p21]

The following lines in the GeneCard text contribute to matching your query:

- GENE: CCR5 (chemokine (C-C motif) receptor 5)
- MOUSE HOMOLOG: Ccr5 (on chromosome 9, 72.00 | Oct 18 2002 | gbaccs: AF019772 AF022990 D83648 U47036 U68565 U83327 X94151 cM)
- SWISSPROT: C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5) (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen)
- SWISSPROT: GENE: CCR5 OR CMKBR5
- HGMD: 1230510 | HGMD entry for CCR5 | mutations
- UNIGENE: Hs.54443 | chemokine (C-C motif) receptor 5 | Build 155: Homo sapiens; Sep 23 2002 | CCR5 | NM\_000579
- LITERATURE: 8663314 | Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha. | SP || 8639485 | Molecular cloning and functional expression of a new human CC-chemokine receptor gene. | HUGO
- GENATLAS: biochem: chemokine CC,beta,receptor 5, expressed in lymphoid organs and cells, with multiple transcripts with 5' end heterogeneity and dual promoter usage, mediating macrophage-tropic strains of HIV-1 entry in CD4+ cells with a reduced risk of AIDS lymphoma in patients with the CCR5-delta 32 mutation, G protein coupled receptor superfamily | disease
- RZPD: id-CCR5

**Display**  
the complete  
GeneCard  
for this  
gene  
(CCL5)

**More like this**

**Gene:** CCL5 = chemokine (C-C motif) ligand 5 [Locus: 17q11.2-q12]

The following lines in the GeneCard text contribute to matching your query:

- SWISSPROT: FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).


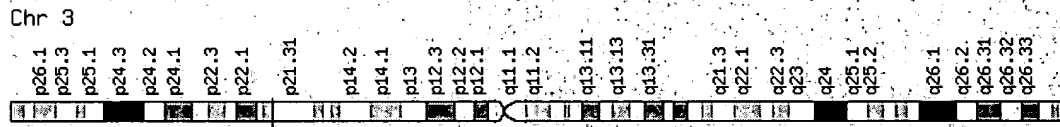
**Display**  
the complete  
GeneCard  
for this  
gene  
(CCL4)

**Gene:** CCL4 = chemokine (C-C motif) ligand 4 [Locus: 17q21-q23]

The following lines in the GeneCard text contribute to matching your query:

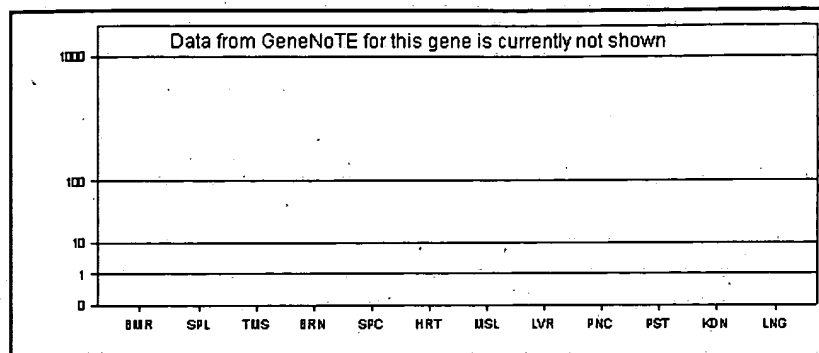
- SWISSPROT: FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES. BINDS TO CCR5 AND TO CCR8. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-BETA INDUCES A

<b>More like this</b>	DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
<b>Display the complete GeneCard for this gene (CCL3)</b>	<b>Gene:</b> CCL3 = chemokine (C-C motif)-ligand 3 [Locus: 17q11-q21]  <b>The following lines in the GeneCard text contribute to matching your query:</b>  - SWISSPROT: FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES. BINDS TO CCR1, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-ALPHA INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
<b>More like this</b>	
<b>Display the complete GeneCard for this gene (BLR1)</b>	<b>Gene:</b> BLR1 = Burkitt lymphoma receptor 1; GTP binding protein (chemokine (C-X-C motif) receptor 5) [Locus: --]  <b>The following lines in the GeneCard text contribute to matching your query:</b>
<b>More like this</b>	
[ This Search Engine uses <u>glimpse</u> and <u>Excite</u> technology ]	
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<b>GeneCard for gene CCR5</b> <b>GC03P045652</b>	Approved <u>UCL/HGNC/HUGO Human Gene Nomenclature database</u> symbol <b>CCR5 (chemokine (C-C motif) receptor 5)</b>		
<b>Aliases and Additional Descriptions</b> (According to GDB, HUGO, and/or SWISS-PROT)	<ul style="list-style-type: none"> <li>• CC-CKR-5</li> <li>• CCCKR5</li> <li>• CKR-5</li> <li>• CKR5</li> <li>• CMKBR5</li> <li>• chemokine (C-C motif) receptor 5</li> <li>• C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5) (HIV-1 fus)</li> </ul>		
<b>Chromosomal Location</b> (According to UDB/GeneLoc and/or HUGO, and/or LocusLink, Genomic Views According to UCSC and Ensembl)	<p><b>Chromosome: 3</b> <u>UDB/GeneLoc gene densities</u></p> <p><b>LocusLink cytogenetic band: 3p21</b> <b>Ensembl cytogenetic band: 3p21.32</b></p> <p><b>Gene in genomic location: bands according to Ensembl, locations according to UDB/GeneL</b></p>  <p><b>Chr 3</b></p> <p><b>Unified DataBase (GeneLoc) location for GC03P045652: (about GC identifiers)</b></p> <p><b>Start:</b> 45,652,489 bp from pter</p> <p><b>End:</b> 45,658,542 bp from pter</p> <p><b>Size:</b> 6,053 bases</p> <p><b>Orientation:</b> plus strand</p> <p><b>Unified DataBase (version 2.5) coordinate (from pter): 50.372 mega bases</b></p> <p><b>Genomic View:</b>  <a href="#">UCSC Golden Path</a> </p>		
<b>Proteins</b> (According to SWISS-PROT and/or MIPS)	<p><b>CKR5 HUMAN</b></p> <ul style="list-style-type: none"> <li>• <b>Size:</b> 352 amino acids; 40524 Da</li> <li>• <b>Function:</b> RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, M SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULA ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFI WITH CD4 FOR PRIMARY NON- SYNCYTIIUM-INDUCING STRAINS (NSI) (MACROI PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.</li> <li>• <b>Subcellular location:</b> Integral membrane protein.</li> <li>• <b>Tissue specificity:</b> FOUND IN PROMYELOCYTIC CELLS.</li> <li>• <b>Ptm:</b> SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.</li> <li>• <b>Ptm:</b> MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED GLYCO</li> <li>• <b>Similarity:</b> BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.</li> </ul> <p><b>MIPS Pedant Viewer:</b> <a href="#">11962</a></p> <p><b>REFSEQ proteins:</b> <a href="#">NP_000570.1</a></p> <p><b>InterPro Domains and Families:</b></p>		

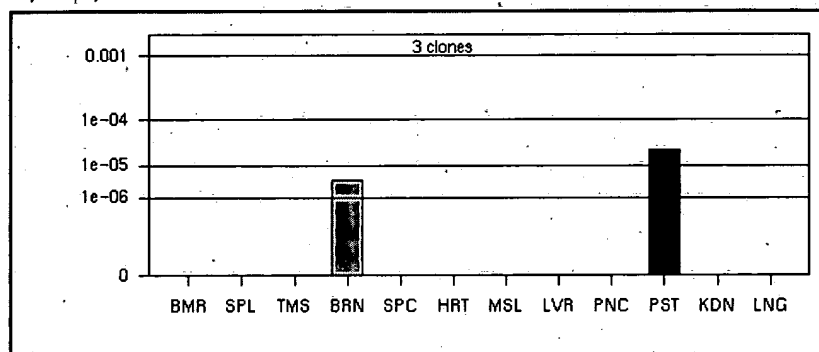
<b>Protein Domains/ Families/Ontologies</b> (According to InterPro, <u>GO</u> , and/or <u>BLOCKS</u> )	<p><u>IPR000276; GPCR Rhodpsn</u></p> <p><u>Graphical View of Domain Structure for SP Entry P51681</u></p> <p><b>Gene Ontology (GO) terms (tree view):</b></p> <p><u>GO:0006935</u> <u>GO:0005887</u> <u>GO:0007267</u> <u>GO:0004872</u> <u>GO:0006954</u> <u>GO:0016021</u> <u>GO:0007186</u> <u>GO:0001584</u> <u>GO:0007204</u> <u>GO:0006968</u> <u>GO:0015026</u> <u>GO:0007203</u> <u>GO:0016493</u> <u>GO:0005768</u> <u>GO:0007125</u> <u>GO:0004945</u> <u>GO:0016494</u></p> <p><b>Blocks protein family:</b> <u>IPB000276 Rhodopsin-like GPCR superfamily</u></p>
<b>Sequences</b> (GenBank/EMBL/DDBJ Accessions According to <u>Unigene</u> or <u>GenBank</u> , RefSeq According to <u>LocusLink</u> , Assembly According to <u>MIPS</u> and/or <u>DOTS</u> )	<p><b>REFSEQ mRNAs:</b> <u>NM_000579.1</u></p> <p><b>Additional Gene/cDNA sequence:</b> <u>AF009962.1</u> <u>AF011500.1</u> <u>AF011501.1</u> <u>AF011502.1</u> <u>AF011503.1</u> <u>AF011505.1</u> <u>AF01150</u> <u>AF011508.1</u> <u>AF011509.1</u> <u>AF011510.1</u> <u>AF011511.1</u> <u>AF011512.1</u> <u>AF011513.1</u> <u>AF01151</u> <u>AF011516.1</u> <u>AF011517.1</u> <u>AF011518.1</u> <u>AF011519.1</u> <u>AF011520.1</u> <u>AF011521.1</u> <u>AF01152</u> <u>AF011524.1</u> <u>AF011525.1</u> <u>AF011526.1</u> <u>AF011527.1</u> <u>AF011528.1</u> <u>AF011531.1</u> <u>AF01153</u> <u>AF011534.1</u> <u>AF011535.1</u> <u>AF011536.1</u> <u>AF031237.1</u> <u>BC038398.1</u> <u>U54994</u> <u>U54994.1</u> <u>U5</u> <u>U57840.1</u> <u>U83326.1</u> <u>U95626.1</u> <u>X91492.1</u></p> <p><b>MIPS assembly:</b> <u>H8606S1</u></p> <p><b>DOTS assembly:</b> <u>DT.311277</u></p> <p><b>Unigene Cluster for CCR5:</b> ( Build 155 Homo sapiens; Sep 23 2002 ) chemokine (C-C motif) receptor 5 <u>Hs.54443</u> [show with all <u>ESTs</u>]</p> <p><b>Unigene Representative Sequence:</b> <u>NM_000579</u></p> <p><b>CCR5 expression in normal human tissues based on proprietary W.I.S DNA array (Gen</b></p>

**Expression  
in Human Tissues**  
(According to  
proprietary W.I.S DNA  
array results  
(GeneNoTE), UniGene  
and/or SOURCE)



- Immune System
- Nervous System
- Muscle
- Secretory Glands
- Other
- Min-max range for

**CCR5 expression in normal human tissues based on quantifying ESTs from various tissues.**



- Tissue**
- BMR Bone marrow
  - SPL Spleen
  - TMS Thymus
  - BRN Brain
  - SPC Spinal cord
  - HRT Heart
  - MSL Skeletal muscle
  - LVR Liver
  - PNC Pancreas
  - PST Prostate
  - KDN Kidney
  - LNG Lung

SOURCE GeneReport for Unigene cluster Hs.54443

**Similar Genes in  
Other Organisms**  
(According to MGD Oct  
18 2002, Stony Brook  
C.elegans-H.sapiens  
Alignment Database  
and/or euGenes)

**Homologues:**

	gene	locus	description	%similarity to human	G
mouse (MGD)	<u>Ccr5</u>	9 (72.00 cM)	chemokine (C-C motif) receptor 5	--	A U
C. elegans (Stony Brook)	B0454.4	--	Caenorhabditis elegans cosmid B0454, complete sequence	42,61%	A

Variants: SWISS-PROT: CKR5 HUMAN

NCBI SNPs: 10/32 selected, not withdrawn, single nucleotide mutations are shown here.  
Click here to see all of them

**SNPs/Variants**  
(According to the NCBI  
SNP Database and to  
SWISS-PROT )

Genomic Data							
SNP ID	Contig Accession	Pos in Contig	Str	5' Flanking Sequence*	3' Flanking Sequence*	Validation	DNA Chg
rs1799987	NT_034534.1	1955693	+	GAAAAAGGGG	CACAGGGTTA	by-submitter	G/A
rs1799988	NT_034534.1	1956017	+	GTAAATAAAC	TTCAGACCAG	by-submitter	T/C
rs3176763	NT_034534.1	1958034	+	CATCTATGTA	GCAATTAAAA	by-frequency	G/T
rs2856762	NT_034534.1	1957090	+	TATGACCTTC	CTGGGACTTG	by-frequency	C/T
rs3087247	NT_034534.1	1955658	+	GGTTGGGGTG	GATAGGGGAT	by-frequency	C/T
rs3087248	NT_034534.1	1955707	+	AGGGTTAATG	GAAGTCCAGG	by-frequency	G/A
rs3087249	NT_034534.1	1956031	+	AGACCAGAGA	CTATTCTCTA	by-frequency	T/C
rs3087250	NT_034534.1	1956126	+	ACTCCACCCT	CTTCAAAAGA	by-frequency	C/A
rs3181036	NT_034534.1	1956317	+	CCATAGAAGA	ATTTGGCAAA	by-frequency	C/T
rs3181037	NT_034534.1	1956688	+	CAAAATTAAT	TTAAATTACA	by-frequency	A/G

\* Lower case letters indicate repetitive or low-complexity sequence

<b>All NCBI SNPs in <u>CCR5</u></b>					
<b>Disorders &amp; Mutations</b> (in which this Gene is Involved, According to OMIM, SWISS-PROT, Genatlas, GeneClinics, HGMD, BCGD, and/or TGDB.)	<b>OMIM ID: 601373</b>  search databases for MIM named disorders: <ul style="list-style-type: none"> <li>• <u>{HIV infection, susceptibility/resistance to} (3)</u></li> </ul> <b>Human Gene Mutation Database entry for CCR5</b>				
<b>Medical News</b> (Possibly Related Articles in <u>Doctor's Guide</u> )	<ul style="list-style-type: none"> <li>• <u>Gene Protects HIV-Infected People From AIDS But Hastens Death</u></li> <li>• <u>Researchers Find Mutation That Slows Down Progression Of HIV</u></li> <li>• <u>Mutant Gene Not Sole Explanation for HIV Non-Progression</u></li> <li>• <u>A Molecular Mechanism that Allows HIV to Enter Human Cells Identified</u></li> <li>• <u>Hidden 'Second Structure' Critical in AIDS Virus Attack</u></li> <li>• <u>Scientists Discover Second Gene Alteration That Slows Progression To AIDS</u></li> </ul>				
<b>Research Articles</b> (in <u>PubMed</u> )	<ul style="list-style-type: none"> <li>• <u>Molecular cloning and functional characterization of a novel human CC chemokine receptor MIP-1alpha.</u></li> <li>• <u>Molecular cloning and functional expression of a new human CC-chemokine receptor</u></li> </ul> <div>Search PubMed for CCR5</div> to find abstracts of <b>research articles</b> containing th				
<b>CCR5 in Other Genome Wide Resources:</b> (According to <u>GDB</u> , <u>LocusLink</u> , <u>euGenes</u> , <u>Ensembl</u> and/or <u>GeneLynx</u> )	<u>GDB: 1230510</u> <u>LocusLink: 1234</u> <u>euGenes: HUgn1234</u> <u>Ensembl: ENSG00000160</u>				
<b>CCR5 in General Databases, Limited Scope</b> (According to <u>HUGE</u> )	--				
<b>CCR5 in Specialized Databases</b> (According to <u>ATLAS</u> , <u>GENATLAS</u> , <u>HORDE</u> , <u>IMGT</u> , <u>MTDB</u> , <u>LEIDEN</u> and/or <u>SWISS-PROT</u> )	<table> <tr> <td><i>name</i></td><td><i>description</i></td></tr> <tr> <td> <b>Genatlas</b> biochemistry entry for CCR5:  chemokine CC,beta,receptor 5,expressed in lymphoid organs and cells,with multiple transcripts with 5' end heterogeneity and dual promoter usage,mediating macrophage-tropic strains of HIV-1 entry in CD4+ cells with a reduced risk of AIDS lymphoma in patients with the CCR5-delta 32 mutation,G protein coupled receptor superfamily </td><td>Links to se</td></tr> </table>	<i>name</i>	<i>description</i>	<b>Genatlas</b> biochemistry entry for CCR5: chemokine CC,beta,receptor 5,expressed in lymphoid organs and cells,with multiple transcripts with 5' end heterogeneity and dual promoter usage,mediating macrophage-tropic strains of HIV-1 entry in CD4+ cells with a reduced risk of AIDS lymphoma in patients with the CCR5-delta 32 mutation,G protein coupled receptor superfamily	Links to se
<i>name</i>	<i>description</i>				
<b>Genatlas</b> biochemistry entry for CCR5: chemokine CC,beta,receptor 5,expressed in lymphoid organs and cells,with multiple transcripts with 5' end heterogeneity and dual promoter usage,mediating macrophage-tropic strains of HIV-1 entry in CD4+ cells with a reduced risk of AIDS lymphoma in patients with the CCR5-delta 32 mutation,G protein coupled receptor superfamily	Links to se				
<b>Services</b> (According to <u>RZPD</u> )	<u>Search RZPD for clones of CCR5</u> Clone collection at the German Human Genome Project				

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Go

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The GeneCards **idea** in brief: **Mining the Internet** for biomedical knowledge and **guiding** the user to it.

Developed at the Crown Human Genome Center & Weizmann Institute of Science

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